

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Deisher, Theresa A.
Conklin, Darrell C.
Raymond, Fenella
Bukowski, Thomas R.
Holderman, Susan D.
Hansen, Birgit
Sheppard, Paul O.
- (ii) TITLE OF THE INVENTION: NOVEL FGF HOMOLOGS
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: ZymoGenetics, Inc.
(B) STREET: 1201 Eastlake Avenue East
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98102
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:

10037922.101904

- (A) NAME: Sawislak, Deborah A
 (B) REGISTRATION NUMBER: 37,438
 (C) REFERENCE/DOCKET NUMBER: 96-20

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 206-442-6672
 (B) TELEFAX: 206-442-6678
 (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...621
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG TAT TCA GCG CCC TCC GCC TGC ACT TGC CTG TGT TTA CAC TTC CTG	48
Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe Leu	
1 5 10 15	
CTG CTG TGC TTC CAG GTA CAG GTG CTG GTT GCC GAG GAG AAC GTG GAC	96
Leu Leu Cys Phe Gln Val Gln Val Leu Val Ala Glu Glu Asn Val Asp	
20 25 30	
TTC CGC ATC CAC GTG GAG AAC CAG ACG CGG GCT CGG GAC GAT GTG AGC	144
Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser	
35 40 45	
CGT AAG CAG CTG CGG CTG TAC CAG CTC TAC AGC CGG ACC AGT GGG AAA	192
Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys	
50 55 60	

1003922 101901

CAC ATC CAG GTC CTG GGC CGC AGG ATC AGT GCC CGC GGC GAG GAT GGG 240
His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly
65 70 75 80

GAC AAG TAT GCC CAG CTC CTA GTG GAG ACA GAC ACC TTC GGT AGT CAA 288
Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser Gln
85 90 95

GTC CGG ATC AAG GGC AAG GAG ACG GAA TTC TAC CTG TGC ATG AAC CGC 336
Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn Arg
100 105 110

AAA GGC AAG CTC GTG GGG AAG CCC GAT GGC ACC AGC AAG GAG TGT GTG 384
Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys Val
115 120 125

TTC ATC GAG AAG GTT CTG GAG AAC AAC TAC ACG GCC CTG ATG TCG GCT 432
Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser Ala
130 135 140

AAG TAC TCC GGC TGG TAC GTG GGC TTC ACC AAG AAG GGG CGG CCG CGG 480
Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro Arg
145 150 155 160

AAG GGC CCC AAG ACC CGG GAG AAC CAG CAG GAC GTG CAT TTC ATG AAG 528
Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met Lys
165 170 175

CGC TAC CCC AAG GGC CAG CCG GAG CTT CAG AAG CCC TTC AAG TAC ACG 576
Arg Tyr Pro Lys Gly Gln Pro Glu Leu Gln Lys Pro Phe Lys Tyr Thr
180 185 190

ACG GTG ACC AAG AGG TCC CGT CGG ATC CGG CCC ACA CAC CCT GCC TAGGC 626
Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Ala
195 200 205

CACCCTGCCG CGGCCCTCAG GTCGCCCTGG CCACACTCAC ACTCCAGAA AACTGCATCA 686
GAGGAATATT TTTACATGAA AAATAAGGAT TTTATTGTTG ACTTGAAACC CCCGATGACA 746
AAAGACTCAC GCAAAGGGAC TGTAAGTCAAC CCACAGGTGC TTGTCTCTCT CTAGGAACAG 806
ACAACCTCTAA ACTCGTCCCC AGAGGAGGAC TTGAATGAGG AAACCAACAC TTTGAGAAAC 866
CAAAGTCCTT TTTCCCAAAG GTTCTGAAAA AAAAAAAAAA AAAAAGTCGA G 917

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe Leu
 1 5 10 15
 Leu Leu Cys Phe Gln Val Gln Val Leu Val Ala Glu Glu Asn Val Asp
 20 25 30
 Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser
 35 40 45
 Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys
 50 55 60
 His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly
 65 70 75 80
 Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser Gln
 85 90 95
 Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn Arg
 100 105 110
 Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys Val
 115 120 125
 Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser Ala
 130 135 140
 Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro Arg
 145 150 155 160
 Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met Lys
 165 170 175
 Arg Tyr Pro Lys Gly Gln Pro Glu Leu Gln Lys Pro Phe Lys Tyr Thr
 180 185 190
 Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Ala
 195 200 205

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC11676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGACTTGACT ACCGAAGGTG TCTG

24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC11677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCGATGTGA GCCGTAAGCA GCT

23

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC12053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCATACTTGT CCCCATCCTC GCCGCG

26

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 621 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10037922 101901

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGTAYWSNG	CNCCNWSNGC	NTGYACNTGY	YTNTGYTNC	AYTTYTNYT	NYTNTGYTTY	60
CARGTNCARG	TNYTNGTNGC	NGARGARAAY	GTNGAYTTYM	GNATHGAYGT	NGARAARCAR	120
ACNMGNGCNM	GNGAYGAYGT	NWSNMGNAAR	CARYTNMGNY	TNTAYCARYT	NTAYWSNMGN	180
ACNWSNGGNA	ARCAYATHCA	RGTNYTNGGN	MGNMGNATHW	SNGCNMGNGG	NGARGAYGGN	240
GAYAARTAYG	CNCARYTNYT	NGTNGARACN	GAYACNTTYG	GNWSNCARGT	NMGNATHAAR	300
GGNAARGARA	CNGARTTYTA	YYTNTGYATG	AAYMGNAARG	GNAARYTNGT	NGGNAARCCN	360
GAYGGNACNW	SNAARGARTG	YGTNTTYATH	GARAARGTNY	TNGARAAYAA	YTAYACNGCN	420
YTATGWSNG	CNAARTAYWS	NGGNTGGTAY	GTNGGNTTYA	CNAARAARGG	NMGNCCNMGN	480
AARGGNCCNA	ARACNMGNGA	RAAYCARCAR	GAYGTNCAYT	TYATGAARMG	NTAYCCNAAR	540
GGNCARCCNG	ARYTNCARAA	RCCNTTYAAR	TAYACNACNG	TNACNAARMG	NWSNMGNMGN	600
ATHMGNCCNA	CNCAYCCNGC	N				621

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC12652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TATTTATCTA GACTGGTTCC GCGTGCCGCC GAGGAGAACG TGGACTT

47

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC12631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10037922-101901

GTATTTGTCTG ACTCAGGCAG GGTGTGTGGG CCG

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC15290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCGAGGAGA ACGTGGACTT CC

22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC15270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TATTTATCTA GAGATGACGA TGACAAGGCC GAGGAGAACG TGGACTT

47

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC13497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

10037922 101901

AGCATTGCTA AAGAAGAAGG TGTAAGCTTG GACAAGAGAG A

41

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZC15131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTGTAAGCT TGGACAAGAG AGAGGAGAAC GTGGACTTCC GCATCCACGT GGAGAACCAG
ACG

60

63

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZC15134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGGCTGTAG AGCTGGTACA GCCGCAGCTG CTTACGGCT

39

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZC13529

T06T0T"2262E00T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTCAGAAGC CCTTCAAGTA CACGACGGTG ACCAAGAGGT CC

42

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC13525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACGACGGTGA CCAAGAGGTC CCGTCGGATC CGGCCACAC ACCCTGCCTA GGGGGAATTC
G

60
61

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC13526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAAACAGGCA GCCCTAGAAT ACTAGTGTCTG ACTCGAGGAT CCGAATTCCC CCTAGGCAGG
G

60
61

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
 (vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC13528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTCAAAAATT ATAAAAATAT CCAAACAGGC AGCCCTAGAA TACT

44

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC15132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGCCGCAGC TGCTTAGCGC TCACATCGTC CCGAGCCCGC GTCTGGTTCT CCACGTGGAT GC

62

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCATTGCTG CTAAAGAAGA AGGTGTAAGC TTGGACAAGA GAGAGGAGAA CGTGGACTTC
 CGCATCCACG TGGAGAACCA GACGCGGGCT CGGGACGATG TGAGCCGTAA GCAGCTGCGG
 CTGTACCAGC TCTACAGCCG G

60

120

141

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid

10037922-101901

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTTCAGAAGC	CCTTCAAGTA	CACGACGGTG	ACCAAGAGGT	CCGTCGGAT	CCGGCCCACA	60
CACCCTGCCT	AGGGGGAATT	CGGATCCTCG	AGTCGACACT	AGTATTCTAG	GGCTGCCTGT	120
TTGGATATTT	TTATAATTTT	TGAG				144

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